# Association between *BRCA1* promoter methylation in peripheral blood DNA and sporadic breast cancer risk in postmenopausal women

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Breast cancer is a complex disease caused by genetic and epigenetic alterations. While pathogenic variants in the BRCA1 gene are well-characterized, its promoter methylation leading to epigenetic silencing has also emerged as a potential alternative mechanism affecting gene expression and tumour development. This study aimed to investigate the association between BRCA1 promoter methylation in peripheral blood DNA and the risk and clinicopathological features of sporadic breast cancer. An existing collection of peripheral blood DNA samples from 30 clinically characterized postmenopausal women with breast cancer and 30 age-matched healthy postmenopausal women was analyzed using methylation-specific polymerase chain reaction (MSP) following DNA bisulfite conversion. Association with clinicopathological features was assessed using descriptive statistics. BRCA1 promoter methylation was detected in 3.3% (1/30) of breast cancer patients and was absent in healthy controls. There was no statistically significant association between BRCA1 promoter methylation and breast cancer risk ($p=0.49$). No significant associations were found with age at menarche, parity, BMI, age at first pregnancy, breastfeeding, or contraceptive use. A significant association was observed with age at menopause ($p=0.002$). Tumour characteristics, such as histological type ($p<0.001$), showed a significant association with methylation status. Tumour grade, stage, lymph node involvement, and hormone receptor status [oestrogen receptor (ER), progesterone receptor (PR), human epidermal growth factor 2 (HER2), and triple negative breast cancer (TNBC)] did not show any associations. The only methylated case involved a grade I tumour with mixed histology. Germline BRCA1 promoter methylation was observed at a low frequency in breast cancer patients and was absent in healthy controls. Its presence in a single early-stage case suggests a potential role in tumour development; however, its low occurrence limits its utility as a predictive biomarker. Larger studies are needed to determine its relevance in risk assessment and prognosis.

**Keywords**: *DNA methylation*, *BRCA1*, *Breast cancer*, *Promoter region*, *Methylation Specific PCR*